

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/548,717

DATE: 05/03/2000  
TIME: 16:30:47

Input Set : A:\200017.app  
Output Set: N:\CRF3\050300\I548717.raw

**Does Not Comply  
Corrected Diskette Needed**

3 <110> APPLICANT: Toyo Boseki Kabushiki Kaisha  
5 <120> TITLE OF INVENTION: METHOD OF EXTRACTING NUCLEIC ACIDS USING PARTICULATE  
6 CARRIER  
8 <130> FILE REFERENCE: 200017  
10 <140> CURRENT APPLICATION NUMBER: US/09/548,717  
11 <141> CURRENT FILING DATE: 2000-04-13  
13 <160> NUMBER OF SEQ ID NOS: 4  
15 <170> SOFTWARE: PatentIn Ver. 2.1  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 24  
19 <212> TYPE: DNA  
20 <213> ORGANISM: Artificial Sequence  
22 <220> FEATURE:  
23 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a  
24 sequence complementary to the nucleotides 102  
25 through 125 of the nucleotide sequence of V.  
26 parahaemolyticus TDH (Thermostable Direct  
27 Haemolysin) gene.  
29 <400> SEQUENCE: 1  
30 ccccggttct gatgagatat tgtt 24  
33 <210> SEQ ID NO: 2  
34 <211> LENGTH: 51  
35 <212> TYPE: DNA  
36 <213> ORGANISM: Artificial Sequence  
38 <220> FEATURE:  
39 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a  
40 sequence complementary to the nucleotides 495-518  
41 of the nucleotide seq. of V. parahaemolyticus TDH  
42 gene, and a promoter sequence for T7-RNA  
43 polymerase.  
45 <400> SEQUENCE: 2  
46 aattcttaata cgactca taaggagacc aatatattac cactaccact a 51  
49 <210> SEQ ID NO: 3  
50 <211> LENGTH: 26  
51 <212> TYPE: DNA  
52 <213> ORGANISM: Artificial Sequence  
54 <220> FEATURE:  
55 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a  
56 sequence complementary to the nucleotides 339  
57 through 364 of the nucleotide sequence of V.  
58 parahaemolyticus TDH (Thermostable Direct  
59 Haemolysin) gene.  
61 <400> SEQUENCE: 3  
62 cggtcattct gctgttgc taaaat 26  
65 <210> SEQ ID NO: 4  
66 <211> LENGTH: 24  
67 <212> TYPE: DNA

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68 <213> ORGANISM: Artificial Sequence  
70 <220> FEATURE:  
71 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a  
72 sequence complementary to the nucleotides 254  
73 through 277 of the nucleotide sequence of V.  
74 parahaemolyticus TDH (Thermostable Direct  
W-OK75 Haemolysin) gene.  
77 <400> SEQUENCE: 4  
W--> 78 caggtactaa ~~an~~ gttgaca tcct

24

see item 10 on Exam Summary Sheet

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/548,717

DATE: 05/03/2000  
TIME: 16:30:48

Input Set : A:\200017.app  
Output Set: N:\CRF3\050300\I548717.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:27 M:259 W: Field exceeds allowed number of lines, <223> Other Information:  
L:43 M:259 W: Field exceeds allowed number of lines, <223> Other Information:  
L:59 M:259 W: Field exceeds allowed number of lines, <223> Other Information:  
L:75 M:259 W: Field exceeds allowed number of lines, <223> Other Information:  
L:78 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:78 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:78 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4

# Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/548,917</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: <b>(2) INFORMATION FOR SEQ ID NO:X:</b> <b>(i) SEQUENCE CHARACTERISTICS:</b> (Do not insert any headings under "SEQUENCE CHARACTERISTICS") <b>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:</b> <b>This sequence is intentionally skipped</b>  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: <b>&lt;210&gt; sequence id number</b> <b>&lt;400&gt; sequence id number</b> <b>000</b>	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" <b>Please explain source of genetic material in &lt;220&gt; to &lt;223&gt; section.</b> (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	<b>Please do not use "Copy to Disk" function of PatentIn version 2.0.</b> This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	